

09/785,215 STN STRATEGY

(FILE 'HOME' ENTERED AT 12:49:46 ON 08 MAY 2006)

FILE 'MEDLINE, BIOSIS, LIFESCI, EMBASE, SCISEARCH, CAPLUS'  
ENTERED AT

12:50:10 ON 08 MAY 2006

L1 38 S JENSEN/AU  
L2 22 S RASMUSSEN/AU  
L3 11 S NIELSEN/AU  
L4 36 DUP REM L1 (2 DUPLICATES REMOVED)  
L5 21 DUP REM L2 (1 DUPLICATE REMOVED)  
L6 11 DUP REM L3 (0 DUPLICATES REMOVED)  
L7 148854 S AMYLOID  
L8 66461 S T HELPER  
L9 138504 S T AND HELPER  
L10 138504 S L8 OR L9  
L11 194 S L7 AND L10  
L12 109 DUP REM L11 (85 DUPLICATES REMOVED)

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	6246	Jensen.in.	US-PGPUB; USPAT	OR	ON	2006/05/08 12:38
L2	2417	Rasmussen.in.	US-PGPUB; USPAT	OR	ON	2006/05/08 12:38
L3	3613	Nielsen.in.	US-PGPUB; USPAT	OR	ON	2006/05/08 12:39
L4	9	L1 and amyloid	US-PGPUB; USPAT	OR	ON	2006/05/08 12:39
L5	4	L2 and amyloid	US-PGPUB; USPAT	OR	ON	2006/05/08 12:39
L6	12	L3 and amyloid	US-PGPUB; USPAT	OR	ON	2006/05/08 12:40
L7	757	amyloid and (T adj helper)	US-PGPUB; USPAT	OR	ON	2006/05/08 12:41
L8	637	L7 and epitope	US-PGPUB; USPAT	OR	ON	2006/05/08 12:41
L9	760	amyloid and (T adj helper)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/08 12:41
L10	639	L9 and epitope	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/08 12:41
S1	1	"6787637".pn.	USPAT	OR	OFF	2006/05/08 12:38

09/785,215 Sequence search  
Public databases

SEQ ID NO: 2

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4058	100.0	770	1	AAP94775	Aap94775 Novel amy
2	4058	100.0	770	2	AAR41546	Aar41546 Mutated A
3	4058	100.0	770	2	AAR63442	Aar63442 Amyloid p
4	4058	100.0	770	2	AAW40130	Aaw40130 Human APP
5	4058	100.0	770	2	AAW97996	Aaw97996 Human amy
6	4058	100.0	770	4	AAE11762	Aae11762 Human amy
7	4058	100.0	770	4	AAE10648	Aae10648 Human amy
8	4058	100.0	770	4	AAE06893	Aae06893 Human amy
9	4058	100.0	770	4	AAE02600	Aae02600 Human amy
10	4058	100.0	770	4	AAU06622	Aau06622 Human par
11	4058	100.0	770	5	ABG94279	Abg94279 Amyloid b
12	4058	100.0	770	5	ABB78609	Abb78609 Human APP
13	4058	100.0	770	5	ABG76936	Abg76936 Humanised
14	4058	100.0	770	5	AAG68317	Aag68317 Human amy
15	4058	100.0	770	5	ABG80591	Abg80591 Human amy

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4058	100.0	770	1	US-08-133-248-8	Sequence 8, Appli
2	4058	100.0	770	1	US-08-231-940-1	Sequence 1, Appli
3	4058	100.0	770	1	US-08-641-774-1	Sequence 1, Appli
4	4058	100.0	770	1	US-08-104-165-3	Sequence 3, Appli
5	4058	100.0	770	2	US-08-464-250-3	Sequence 3, Appli
6	4058	100.0	770	2	US-08-464-250-3	Sequence 3, Appli
7	4058	100.0	770	2	US-09-548-372D-55	Sequence 55, Appl
8	4058	100.0	770	2	US-09-548-367D-55	Sequence 55, Appl
9	4058	100.0	770	2	US-09-551-853D-55	Sequence 55, Appl
10	4058	100.0	770	2	US-08-665-649-3	Sequence 3, Appli
11	4058	100.0	770	2	US-09-416-901B-55	Sequence 55, Appl
12	4058	100.0	770	2	US-09-548-376D-55	Sequence 55, Appl
13	4058	100.0	770	2	US-09-149-718-6	Sequence 6, Appli
14	4058	100.0	770	2	US-09-794-927A-55	Sequence 55, Appl
15	4058	100.0	770	2	US-09-548-373D-55	Sequence 55, Appl

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4058	100.0	770	3	US-09-794-927-55	Sequence 55, Appl
2	4058	100.0	770	3	US-09-795-847-55	Sequence 55, Appl
3	4058	100.0	770	3	US-09-794-743-55	Sequence 55, Appl
4	4058	100.0	770	3	US-09-794-748-55	Sequence 55, Appl
5	4058	100.0	770	3	US-09-904-987-2	Sequence 2, Appli
6	4058	100.0	770	3	US-09-794-925-55	Sequence 55, Appl
7	4058	100.0	770	3	US-09-681-442-55	Sequence 55, Appl
8	4058	100.0	770	3	US-09-149-718-6	Sequence 6, Appli
9	4058	100.0	770	3	US-09-785-215-2	Sequence 2, Appli
10	4058	100.0	770	3	US-09-848-616-172	Sequence 172, App
11	4058	100.0	770	3	US-09-869-414-55	Sequence 55, Appl
12	4058	100.0	770	3	US-09-548-366-55	Sequence 55, Appl
13	4058	100.0	770	4	US-10-217-584-5	Sequence 5, Appli
14	4058	100.0	770	4	US-10-204-362-2	Sequence 2, Appli
15	4058	100.0	770	4	US-10-169-580-5	Sequence 5, Appli

# SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	4058	100.0	770	9	US-10-982-545-15	Sequence 15, Appl
2	4058	100.0	770	9	US-10-789-273-38	Sequence 38, Appl
3	3943.5	97.2	751	11	US-11-220-372-313	Sequence 313, App
4	1981.5	48.8	763	9	US-10-821-234-1619	Sequence 1619, Ap
5	1159.5	28.6	650	11	US-11-051-720-1439	Sequence 1439, Ap
6	1011	24.9	619	11	US-11-051-720-1353	Sequence 1353, Ap
7	1010.5	24.9	519	11	US-11-051-720-1350	Sequence 1350, Ap
8	1010.5	24.9	541	11	US-11-051-720-1351	Sequence 1351, Ap
9	1010.5	24.9	544	11	US-11-051-720-1352	Sequence 1352, Ap
10	998.5	24.6	498	11	US-11-051-720-1355	Sequence 1355, Ap
11	975	24.0	597	11	US-11-051-720-1354	Sequence 1354, Ap
12	922.5	22.7	588	11	US-11-051-720-1356	Sequence 1356, Ap
13	910.5	22.4	505	11	US-11-051-720-1357	Sequence 1357, Ap
14	531	13.1	103	9	US-10-677-076-2	Sequence 2, Appli
15	517	12.7	100	11	US-11-243-578-1	Sequence 1, Appli

Result No.	Score	Query Match	Length	DB	ID	Description
1	4058	100.0	770	1	QRHUA4	Alzheimer's diseas
2	3590.5	88.5	695	1	A49795	Alzheimer's diseas
3	3493.5	86.1	695	2	S00550	Alzheimer's diseas
4	3468.5	85.5	695	2	A27485	Alzheimer's diseas
5	3403.5	83.9	747	2	JH0773	Alzheimer's diseas
6	2446.5	60.3	484	4	A32761	hypothetical Alzhe
7	1981.5	48.8	763	2	A49321	amyloid beta (A4)
8	1971.5	48.6	765	2	S42880	amyloid precursor-
9	1956.5	48.2	751	2	A49974	beta-amyloid precu
10	1150.5	28.4	653	2	A46362	amyloid precursor-
11	1112.5	27.4	511	2	JC1404	CDEI-box DNA-bindi
12	785	19.3	686	2	T15795	hypothetical prote
13	737.5	18.2	886	2	A32758	beta-amyloid-like
14	706	17.4	246	2	S38344	CDEI-binding prote
15	501	12.3	100	2	A32282	Alzheimer's diseas

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4058	100.0	770	1	A4_HUMAN	P05067 h amyloid b
2	4054	99.9	770	1	A4_PANTR	Q51s80 p amyloid b
3	4040	99.6	770	1	A4_MACFA	P53601 m amyloid b
4	3981	98.1	770	1	A4_PIG	P79307 s amyloid b
5	3952	97.4	770	1	A4_CAVPO	Q60495 c amyloid b
6	3946	97.2	770	2	Q6RH30_CANFA	Q6rh30 canis famil
7	3943.5	97.2	751	2	Q6GSC0_HUMAN	Q6gsc0 homo sapien
8	3937	97.0	770	1	A4_RAT	P08592 r amyloid b
9	3937	97.0	770	2	Q547B7_RAT	Q547b7 rattus norv
10	3936	97.0	770	2	Q56JK6_CANFA	Q56jk6 canis famil
11	3934.5	97.0	751	2	Q4R4R8_MACFA	Q4r4r8 macaca fasc
12	3927	96.8	770	2	Q53ZT3_MOUSE	Q53zt3 mus musculu
13	3923	96.7	770	1	A4_MOUSE	P12023 m amyloid b
14	3921.5	96.6	751	1	A4_SAISC	Q95241 s amyloid b
15	3848.5	94.8	751	2	Q6RH28_CANFA	Q6rh28 canis famil

Residues 630-770 SEQ ID NO: 2

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	725	100.0	264	1	AAP90497	Aap90497 Protein s
2	725	100.0	695	1	AAP81692	Aap81692 Sequence
3	725	100.0	695	2	AAR14046	Aar14046 Amyloid p
4	725	100.0	695	2	AAR26338	Aar26338 APP695. 3

5	725	100.0	695	2	AAR58923	Aar58923 Mouse amy
6	725	100.0	695	2	AAR58920	Aar58920 Amyloid p
7	725	100.0	695	2	AAY20233	Aay20233 Human bet
8	725	100.0	695	2	AAY49690	Aay49690 Human bet
9	725	100.0	695	2	AAY07221	Aay07221 Amyloid p
10	725	100.0	695	3	AAy88434	Aay88434 Human APP
11	725	100.0	695	3	AAy44705	Aay44705 Human bet
12	725	100.0	695	4	AAe10632	Aae10632 Human wil
13	725	100.0	695	4	AAe06862	Aae06862 Human wil
14	725	100.0	695	4	AAe02584	Aae02584 Human amy
15	725	100.0	695	4	AAU06606	Aau06606 Human Amy

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	725	100.0	264	1	US-07-990-893-5	Sequence 5, Appli
2	725	100.0	695	1	US-08-371-930-27	Sequence 27, Appl
3	725	100.0	695	1	US-08-123-702-2	Sequence 2, Appli
4	725	100.0	695	1	US-08-104-165-1	Sequence 1, Appli
5	725	100.0	695	2	US-08-464-250-1	Sequence 1, Appli
6	725	100.0	695	2	US-08-464-250-1	Sequence 1, Appli
7	725	100.0	695	2	US-09-458-481B-7	Sequence 7, Appli
8	725	100.0	695	2	US-09-458-481B-8	Sequence 8, Appli
9	725	100.0	695	2	US-09-548-372D-10	Sequence 10, Appl
10	725	100.0	695	2	US-09-548-367D-10	Sequence 10, Appl
11	725	100.0	695	2	US-09-551-853D-10	Sequence 10, Appl
12	725	100.0	695	2	US-09-415-099-6	Sequence 6, Appli
13	725	100.0	695	2	US-09-416-901B-10	Sequence 10, Appl
14	725	100.0	695	2	US-09-548-376D-10	Sequence 10, Appl
15	725	100.0	695	2	US-09-149-718-2	Sequence 2, Appli

Result No.	Score	% Query Match	Length	DB	ID	Description
1	725	100.0	695	3	US-09-794-927-10	Sequence 10, Appl
2	725	100.0	695	3	US-09-795-847-10	Sequence 10, Appl
3	725	100.0	695	3	US-09-794-743-10	Sequence 10, Appl
4	725	100.0	695	3	US-09-794-748-10	Sequence 10, Appl
5	725	100.0	695	3	US-09-794-925-10	Sequence 10, Appl
6	725	100.0	695	3	US-09-681-442-10	Sequence 10, Appl
7	725	100.0	695	3	US-09-149-718-2	Sequence 2, Appli
8	725	100.0	695	3	US-09-869-414-10	Sequence 10, Appl
9	725	100.0	695	3	US-09-548-366-10	Sequence 10, Appl
10	725	100.0	695	3	US-09-998-491-1	Sequence 1, Appli
11	725	100.0	695	4	US-10-169-580-3	Sequence 3, Appli
12	725	100.0	695	4	US-10-357-935-1	Sequence 1, Appli
13	725	100.0	695	4	US-10-427-208-45	Sequence 45, Appl
14	725	100.0	695	4	US-10-652-927-10	Sequence 10, Appl
15	725	100.0	695	4	US-10-652-830-10	Sequence 10, Appl

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	725	100.0	751	11	US-11-220-372-313	Sequence 313, App
2	725	100.0	770	9	US-10-982-545-15	Sequence 15, Appl
3	725	100.0	770	9	US-10-789-273-38	Sequence 38, Appl
4	531	73.2	103	9	US-10-677-076-2	Sequence 2, Appli
5	517	71.3	100	11	US-11-243-578-1	Sequence 1, Appli
6	517	71.3	108	11	US-11-243-578-9	Sequence 9, Appli
7	516	71.2	100	11	US-11-243-578-2	Sequence 2, Appli
8	516	71.2	100	11	US-11-243-578-3	Sequence 3, Appli
9	516	71.2	108	11	US-11-243-578-10	Sequence 10, Appl
10	516	71.2	108	11	US-11-243-578-11	Sequence 11, Appl
11	514	70.9	100	11	US-11-243-578-7	Sequence 7, Appli
12	514	70.9	108	11	US-11-243-578-15	Sequence 15, Appl
13	513	70.8	100	11	US-11-243-578-6	Sequence 6, Appli

14	513	70.8	108	11	US-11-243-578-14	Sequence 14, Appl
15	512	70.6	100	11	US-11-243-578-5	Sequence 5, Appli

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	725	100.0	695	1	A49795	Alzheimer's diseas
2	725	100.0	770	1	QRHUA4	Alzheimer's diseas
3	706	97.4	695	2	A27485	Alzheimer's diseas
4	706	97.4	695	2	S00550	Alzheimer's diseas
5	700	96.6	747	2	JH0773	Alzheimer's diseas
6	411	56.7	82	2	PQ0438	Alzheimer's diseas
7	290	40.0	511	2	JC1404	CDEI-box DNA-bindi
8	290	40.0	751	2	A49974	beta-amyloid precu
9	283	39.0	57	2	A60045	Alzheimer's diseas
10	283	39.0	57	2	F60045	Alzheimer's diseas
11	283	39.0	57	2	D60045	Alzheimer's diseas
12	283	39.0	57	2	E60045	Alzheimer's diseas
13	283	39.0	57	2	G60045	Alzheimer's diseas
14	283	39.0	57	2	B60045	Alzheimer's diseas
15	282.5	39.0	763	2	A49321	amyloid beta (A4)

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	725	100.0	695	2	Q5R477_PONPY	Q5r477 pongo pygma
2	725	100.0	695	2	Q6RH29_CANFA	Q6rh29 canis famil
3	725	100.0	695	2	Q56JK3_CANFA	Q56jk3 canis famil
4	725	100.0	714	2	Q56JK4_CANFA	Q56jk4 canis famil
5	725	100.0	751	1	A4_SAIISC	Q95241 s amyloid b
6	725	100.0	751	2	Q6GSC0_HUMAN	Q6gsc0 homo sapien
7	725	100.0	751	2	Q6RH28_CANFA	Q6rh28 canis famil
8	725	100.0	751	2	Q56JK5_CANFA	Q56jk5 canis famil
9	725	100.0	751	2	Q4R4R8_MACFA	Q4r4r8 macaca fasc
10	725	100.0	770	1	A4_CAVPO	Q60495 c amyloid b
11	725	100.0	770	1	A4_HUMAN	P05067 h amyloid b
12	725	100.0	770	1	A4_MACFA	P53601 m amyloid b
13	725	100.0	770	1	A4_PANTR	Q5is80 p amyloid b
14	725	100.0	770	1	A4_PIG	P79307 s amyloid b
15	725	100.0	770	2	Q6RH30_CANFA	Q6rh30 canis famil

SEQ ID NO: 4

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	74	100.0	15	2	AAR06310	Aar06310 Tetanus t
2	74	100.0	15	2	ADB87354	Adb87354 Cytotoxic
3	74	100.0	15	2	AAW11505	Aaw11505 Tetanus t
4	74	100.0	15	2	AAW35506	Aaw35506 Universal
5	74	100.0	15	2	AAW71321	Aaw71321 Universal
6	74	100.0	15	2	AAW67033	Aaw67033 Tetanus t
7	74	100.0	15	2	AAW67578	Aaw67578 T-cell ep
8	74	100.0	15	2	AAW04051	Aay04051 T-Helper
9	74	100.0	15	2	AAW73220	Aaw73220 Tetanus t
10	74	100.0	15	3	AAW92625	Aay92625 Foreign e
11	74	100.0	15	3	AAW70300	Aay70300 Clostridi
12	74	100.0	15	3	AAW84427	Aay84427 Amino aci
13	74	100.0	15	3	AAW82637	Aay82637 Tetanus t
14	74	100.0	15	3	AAW44763	Aay44763 Tetanus t
15	74	100.0	15	3	AAB45511	Aab45511 Tetanus P

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			

1	74	100.0	15	1	US-08-319-704-10	Sequence 10, Appl
2	74	100.0	15	1	US-08-661-052-6	Sequence 6, Appli
3	74	100.0	15	1	US-08-460-502-7	Sequence 7, Appli
4	74	100.0	15	2	US-09-046-373-2	Sequence 2, Appli
5	74	100.0	15	2	US-09-188-082-6	Sequence 6, Appli
6	74	100.0	15	2	US-09-364-088-6	Sequence 6, Appli
7	74	100.0	15	2	US-09-102-716-6	Sequence 6, Appli
8	74	100.0	15	2	US-09-148-711A-7	Sequence 7, Appli
9	74	100.0	15	2	US-08-716-249-4	Sequence 4, Appli
10	74	100.0	15	2	US-09-362-731A-13	Sequence 13, Appl
11	74	100.0	15	2	US-09-396-937-34	Sequence 34, Appl
12	74	100.0	15	2	US-09-405-986A-1	Sequence 1, Appli
13	74	100.0	15	2	US-09-724-961-49	Sequence 49, Appl
14	74	100.0	15	2	US-09-556-818-23	Sequence 23, Appl
15	74	100.0	15	2	US-09-580-018-49	Sequence 49, Appl

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	74	100.0	15	3	US-09-862-849-2	Sequence 2, Appli
2	74	100.0	15	3	US-09-785-215-4	Sequence 4, Appli
3	74	100.0	15	3	US-09-405-986-1	Sequence 1, Appli
4	74	100.0	15	4	US-10-114-716A-2	Sequence 2, Appli
5	74	100.0	15	4	US-10-204-362-4	Sequence 4, Appli
6	74	100.0	15	4	US-10-223-711-7	Sequence 7, Appli
7	74	100.0	15	4	US-10-237-656-13	Sequence 13, Appl
8	74	100.0	15	4	US-10-223-809A-4	Sequence 4, Appli
9	74	100.0	15	4	US-10-261-446-19	Sequence 19, Appl
10	74	100.0	15	4	US-10-239-313A-618	Sequence 618, App
11	74	100.0	15	4	US-10-295-074-3	Sequence 3, Appli
12	74	100.0	15	4	US-10-372-111-7	Sequence 7, Appli
13	74	100.0	15	4	US-10-668-400-1	Sequence 1, Appli
14	74	100.0	15	4	US-10-261-445B-19	Sequence 19, Appl
15	74	100.0	15	4	US-10-664-801-34	Sequence 34, Appl

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	74	100.0	15	9	US-10-866-120-1	Sequence 1, Appli
2	74	100.0	15	11	US-11-202-516-12	Sequence 12, Appl
3	74	100.0	15	11	US-11-185-907-9	Sequence 9, Appli
4	74	100.0	16	11	US-11-185-907-16	Sequence 16, Appl
5	74	100.0	16	11	US-11-185-907-18	Sequence 18, Appl
6	74	100.0	16	11	US-11-185-907-31	Sequence 31, Appl
7	74	100.0	17	9	US-10-723-207-63	Sequence 63, Appl
8	74	100.0	17	11	US-11-090-497-14	Sequence 14, Appl
9	74	100.0	18	11	US-11-084-554-9	Sequence 9, Appli
10	74	100.0	18	11	US-11-136-250-9	Sequence 9, Appli
11	74	100.0	22	11	US-11-185-907-34	Sequence 34, Appl
12	74	100.0	22	11	US-11-185-907-37	Sequence 37, Appl
13	74	100.0	22	11	US-11-185-907-53	Sequence 53, Appl
14	74	100.0	25	11	US-11-202-516-16	Sequence 16, Appl
15	74	100.0	25	11	US-11-202-516-17	Sequence 17, Appl

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	74	100.0	1315	1	BTCLTN	tentoxilysin (EC 3
2	44.5	60.1	244	2	S29982	class II histocomp
3	44	59.5	66	2	S31029	gene 84 protein -
4	43	58.1	180	2	G86826	diamine N-acetyltr
5	43	58.1	899	2	T42976	hypothetical prote
6	42.5	57.4	1060	2	S06286	major merozoite su
7	42.5	57.4	1086	2	S16752	major merozoite su

8	42.5	57.4	1701	2	A26868	major merozoite su
9	42.5	57.4	1701	2	A54498	major merozoite su
10	42.5	57.4	1726	1	SAZQGM	major merozoite su
11	42.5	57.4	1726	2	A45948	major merozoite su
12	42	56.8	1333	2	S38635	blastopia polyprot
13	41	55.4	123	2	G48677	Ig heavy chain V-D
14	41	55.4	447	2	H97146	siderophore/Surfac
15	41	55.4	899	2	G36812	hypothetical prote

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	1310	2	Q93N27_CLOTE	Q93n27 clostridium
2	74	100.0	1314	1	TETX_CLOTE	P04958 clostridium
3	46	62.2	447	1	ENO_CANBF	Q7vqh3 candidatus
4	46	62.2	880	1	SYA_ENTFA	Q835j8 enterococcu
5	45	60.8	761	2	Q4N7Q0_THEPA	Q4n7q0 theileria p
6	44.5	60.1	60	2	Q31585_SALSA	Q31585 salmo salar
7	44.5	60.1	71	2	Q9XRJ9_9TELE	Q9xrx9 salvelinus
8	44.5	60.1	85	2	Q95HY1_SALSA	Q95hy1 salmo salar
9	44.5	60.1	85	2	Q95IS2_SALSA	Q95is2 salmo salar
10	44.5	60.1	86	2	Q95HX4_SALSA	Q95hx4 salmo salar
11	44.5	60.1	244	2	Q31590_SALSA	Q31590 salmo salar
12	44	59.5	66	1	VG84_BPML5	Q05301 mycobacteri
13	44	59.5	546	2	Q9XG37_GUITH	Q9xg37 guillardia
14	43.5	58.8	67	2	Q31578_SALSA	Q31578 salmo salar
15	43	58.1	180	2	Q9CF66_LACLA	Q9cf66 lactococcus

SEQ ID NO: 6

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	112	100.0	21	2	AAR11896	Aar11896 Immunogen
2	112	100.0	21	2	AAW06130	Aaw06130 Tetanus t
3	112	100.0	21	2	AAR88397	Aar88397 T-cell an
4	112	100.0	21	2	AAW46449	Aaw46449 Broad ran
5	112	100.0	21	2	AAW67034	Aaw67034 Tetanus t
6	112	100.0	21	2	AAW67579	Aaw67579 T-cell ep
7	112	100.0	21	2	AAW73222	Aaw73222 Tetanus t
8	112	100.0	21	3	AAY92626	Aay92626 Foreign e
9	112	100.0	21	3	AAY99876	Aay99876 Tetanus t
10	112	100.0	21	3	AAy84428	Aay84428 Amino aci
11	112	100.0	21	3	AAy49260	Aay49260 CD4+ T ce
12	112	100.0	21	3	AAB45512	Aab45512 Tetanus P
13	112	100.0	21	4	AAE11764	Aae11764 Clostridi
14	112	100.0	21	4	AAB49072	Aab49072 Tetanus t
15	112	100.0	21	4	AAB46173	Aab46173 Tetanus t

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	112	100.0	21	1	US-07-610-525-1	Sequence 1, Appli
2	112	100.0	21	1	US-08-661-052-12	Sequence 12, Appl
3	112	100.0	21	1	US-08-460-502-8	Sequence 8, Appli
4	112	100.0	21	1	US-08-724-774B-5	Sequence 5, Appli
5	112	100.0	21	2	US-09-089-595-5	Sequence 5, Appli
6	112	100.0	21	2	US-09-382-855-5	Sequence 5, Appli
7	112	100.0	21	2	US-09-183-714B-5	Sequence 5, Appli
8	112	100.0	21	2	US-09-188-082-12	Sequence 12, Appl
9	112	100.0	21	2	US-09-171-969-10	Sequence 10, Appl
10	112	100.0	21	2	US-09-364-088-12	Sequence 12, Appl
11	112	100.0	21	2	US-09-642-281-5	Sequence 5, Appli
12	112	100.0	21	2	US-09-102-716-12	Sequence 12, Appl
13	112	100.0	21	2	US-08-432-483A-3	Sequence 3, Appli



14	112	100.0	21	2	US-09-148-711A-8	Sequence 8, Appli
15	112	100.0	21	2	US-09-589-717-5	Sequence 5, Appli

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	112	100.0	21	3	US-09-943-548-3	Sequence 3, Appli
2	112	100.0	21	3	US-09-848-834A-4	Sequence 4, Appli
3	112	100.0	21	3	US-09-785-215-6	Sequence 6, Appli
4	112	100.0	21	3	US-09-405-986-2	Sequence 2, Appli
5	112	100.0	21	3	US-09-943-334-3	Sequence 3, Appli
6	112	100.0	21	4	US-10-204-362-6	Sequence 6, Appli
7	112	100.0	21	4	US-10-339-522-3	Sequence 3, Appli
8	112	100.0	21	4	US-10-223-711-8	Sequence 8, Appli
9	112	100.0	21	4	US-10-223-809A-6	Sequence 6, Appli
10	112	100.0	21	4	US-10-261-208-5	Sequence 5, Appli
11	112	100.0	21	4	US-10-295-074-5	Sequence 5, Appli
12	112	100.0	21	4	US-10-372-111-8	Sequence 8, Appli
13	112	100.0	21	4	US-10-668-400-2	Sequence 2, Appli
14	112	100.0	21	4	US-10-664-801-35	Sequence 35, Appli
15	112	100.0	21	4	US-10-699-517-10	Sequence 10, Appli

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	112	100.0	21	11	US-11-202-516-14	Sequence 14, Appli
2	112	100.0	21	11	US-11-185-907-10	Sequence 10, Appli
3	112	100.0	22	11	US-11-185-907-17	Sequence 17, Appli
4	112	100.0	28	11	US-11-185-907-35	Sequence 35, Appli
5	112	100.0	31	11	US-11-202-516-18	Sequence 18, Appli
6	112	100.0	31	11	US-11-202-516-19	Sequence 19, Appli
7	112	100.0	31	11	US-11-202-516-20	Sequence 20, Appli
8	112	100.0	37	11	US-11-185-907-19	Sequence 19, Appli
9	112	100.0	43	11	US-11-185-907-36	Sequence 36, Appli
10	112	100.0	44	11	US-11-185-907-51	Sequence 51, Appli
11	112	100.0	51	11	US-11-185-907-52	Sequence 52, Appli
12	112	100.0	77	11	US-11-185-907-30	Sequence 30, Appli
13	112	100.0	79	11	US-11-185-907-49	Sequence 49, Appli
14	112	100.0	106	11	US-11-185-907-29	Sequence 29, Appli
15	112	100.0	209	9	US-10-518-701-6	Sequence 6, Appli

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	112	100.0	1315	1	BTCLTN	tentoxilysin (EC 3
2	62	55.4	1268	2	S33411	botulinum neurotox
3	61	54.5	366	2	S48110	neurotoxin type F
4	61	54.5	369	2	S48109	neurotoxin type F
5	61	54.5	1274	2	I40813	neurotoxin type F
6	61	54.5	1297	2	S39791	neurotoxin - Clost
7	59	52.7	1296	1	BTCLAB	bontoxilysin (EC 3
8	58	51.8	1291	1	A48940	bontoxilysin (EC 3
9	58	51.8	1291	2	I40631	non-proteolytic bo
10	56	50.0	367	2	S48106	neurotoxin type E
11	56	50.0	1251	2	JH0256	botulinum neurotox
12	56	50.0	1252	2	S21178	botulinum neurotox
13	56	50.0	1296	2	I40645	botulinum neurotox
14	52	46.4	449	2	S23158	nucleocapsid prote
15	52	46.4	464	1	MNVUWC	nonstructural prot

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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1	112	100.0	451	2	Q9LA13_CLOTE	Q9la13	clostridium
2	112	100.0	1310	2	Q93N27_CLOTE	Q93n27	clostridium
3	112	100.0	1314	1	TETX_CLOTE	P04958	clostridium
4	62	55.4	1268	2	Q45851_9CLOT	Q45851	clostridium
5	61	54.5	366	2	Q79AH9_CLOBO	Q79ah9	clostridium
6	61	54.5	1274	1	BXF_CLOBO	P30996	clostridium
7	61	54.5	1278	2	Q57236_CLOBO	Q57236	clostridium
8	61	54.5	1296	1	BXG_CLOBO	Q60393	clostridium
9	59	52.7	1295	1	BXA1_CLOBO	P10845	clostridium
10	59	52.7	1296	2	Q7B8V4_CLOBO	Q7b8v4	clostridium
11	58	51.8	361	2	Q45846_CLOBO	Q45846	clostridium
12	58	51.8	361	2	Q45848_CLOBO	Q45848	clostridium
13	58	51.8	441	2	Q9X708_CLOBO	Q9x708	clostridium
14	58	51.8	1290	1	BXB_CLOBO	P10844	clostridium
15	58	51.8	1291	2	Q08077_CLOBO	Q08077	clostridium